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RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/073,138

DATE: 07/25/2002
TIME: 14:33:23

Input Set : N:\Crf3\RULE60\10073138.raw
Output Set: N:\CRF3\07252002\J073138.raw

ENTERED

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: ANDERSON, Darrell R.
6 HANNA, Nabil
7 BRAMS, Peter

9 (ii) TITLE OF INVENTION: IDENTIFICATION OF UNIQUE BINDING
10 INTERACTIONS BETWEEN CERTAIN ANTIBODIES AND THE HUMAN

B7.1 AND B7.2 CO-STIMULATORY ANTIGENS

11 (iii) NUMBER OF SEQUENCES: 6

13 (iv) CORRESPONDENCE ADDRESS:
15 (A) ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
16 (B) STREET: P.O. Box 1404
17 (C) CITY: Alexandria
18 (D) STATE: Virginia
19 (E) COUNTRY: United States
20 (F) ZIP: 22313-1404

23 (v) COMPUTER READABLE FORM:

24 (A) MEDIUM TYPE: Floppy disk
25 (B) COMPUTER: IBM PC compatible
26 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
27 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

29 (vi) CURRENT APPLICATION DATA:

30 (A) APPLICATION NUMBER: US/10/073,138
C--> 31 (B) FILING DATE: 13-Feb-2002

C--> 32 (C) CLASSIFICATION:

34 (vii) PRIOR APPLICATION DATA:

35 (A) APPLICATION NUMBER: US/08/746,361
36 (B) FILING DATE: 08-NOV-1996
38 (A) APPLICATION NUMBER: US 08/487,550
39 (B) FILING DATE: 07-JUN-1995

41 (viii) ATTORNEY/AGENT INFORMATION:

42 (A) NAME: Teskin, Robin L.
43 (B) REGISTRATION NUMBER: 35,030
44 (C) REFERENCE/DOCKET NUMBER: 012712-256

46 (ix) TELECOMMUNICATION INFORMATION:

47 (A) TELEPHONE: (703) 836-6620
48 (B) TELEFAX: (703) 836-2021

51 (2) INFORMATION FOR SEQ ID NO: 1:

53 (i) SEQUENCE CHARACTERISTICS:

54 (A) LENGTH: 705 base pairs
55 (B) TYPE: nucleic acid
56 (C) STRANDEDNESS: single
57 (D) TOPOLOGY: linear

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59 (ii) MOLECULE TYPE: DNA (genomic)
 61 (ix) FEATURE:
 62 (A) NAME/KEY: CDS
 63 (B) LOCATION: 1..705
 65 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
 67 ATG AGG GTC CCC GCT CAG CTC CTG GGG CTC CTG CTC TGG CTC CCA 48
 68 Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Trp Leu Pro
 69 1 5 10 15
 71 GGT GCA CGA TGT GCC TAT GAA CTG ACT CAG CCA CCC TCG GTG TCA GTG 96
 72 Gly Ala Arg Cys Ala Tyr Glu Leu Thr Gln Pro Pro Ser Val Ser Val
 73 20 25 30
 75 TCC CCA GGA CAG ACG GCC AGG ATC ACC TGT GGG GGA GAC AAC AGT AGA 144
 76 Ser Pro Gly Gln Thr Ala Arg Ile Thr Cys Gly Asp Asn Ser Arg
 77 35 40 45
 79 AAT GAA TAT GTC CAC TGG TAC CAG CAG AAG CCA GCG CGG GCC CCT ATA 192
 80 Asn Glu Tyr Val His Trp Tyr Gln Gln Lys Pro Ala Arg Ala Pro Ile
 81 50 55 60
 83 CTG GTC ATC TAT GAT GAT AGT GAC CGG CCC TCA GGG ATC CCT GAG CGA 240
 84 Leu Val Ile Tyr Asp Asp Ser Asp Arg Pro Ser Gly Ile Pro Glu Arg
 85 65 70 75 80
 87 TTC TCT GGC TCC AAA TCA GGG AAC ACC GCC ACC CTG ACC ATC AAC GGG 288
 88 Phe Ser Gly Ser Lys Ser Gly Asn Thr Ala Thr Leu Thr Ile Asn Gly
 89 85 90 95
 91 GTC GAG GCC GGG GAT GAG GCT GAC TAT TAC TGT CAG GTG TGG GAC AGG 336
 92 Val Glu Ala Gly Asp Glu Ala Asp Tyr Tyr Cys Gln Val Trp Asp Arg
 93 100 105 110
 95 GCT AGT GAT CAT CCG GTC TTC GGA GGA GGG ACC CGG GTG ACC GTC CTA 384
 96 Ala Ser Asp His Pro Val Phe Gly Gly Thr Arg Val Thr Val Leu
 97 115 120 125
 99 GGT CAG CCC AAG GCT GCC CCC TCG GTC ACT CTG TTC CCG CCC TCC TCT 432
 100 Gly Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser
 101 130 135 140
 103 GAG GAG CTT CAA GCC AAC AAG GCC ACA CTG GTG TGT CTC ATA AGT GAC 480
 104 Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp
 105 145 150 155 160
 107 TTC TAC CCG GGA GCC GTG ACA GTG GCC TGG AAG GCA GAT AGC AGC CCC 528
 108 Phe Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro
 109 165 170 175
 111 GTC AAG GCG GGA GTG GAG ACC ACC ACA CCC TCC AAA CAA AGC AAC AAC 576
 112 Val Lys Ala Gly Val Glu Thr Thr Pro Ser Lys Gln Ser Asn Asn
 113 180 185 190
 115 AAG TAC GCG GCC AGC AGC TAC CTG AGC CTG ACG CCT GAG CAG TGG AAG 624
 116 Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys
 117 195 200 205
 119 TCC CAC AGA AGC TAC AGC TGC CAG GTC ACG CAT GAA GGG AGC ACC GTG 672
 120 Ser His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val
 121 210 215 220
 123 GAG AAG ACA GTG GCC CCT ACA GAA TGT TCA TGA 705
 124 Glu Lys Thr Val Ala Pro Thr Glu Cys Ser *

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W--> 125	225	230	235	
128	(2)	INFORMATION FOR SEQ ID NO: 2:		
130	(i)	SEQUENCE CHARACTERISTICS:		
131	(A)	LENGTH: 1431 base pairs		
132	(B)	TYPE: nucleic acid		
133	(C)	STRANDEDNESS: single		
134	(D)	TOPOLOGY: linear		
136	(ii)	MOLECULE TYPE: DNA (genomic)		
138	(ix)	FEATURE:		
139	(A)	NAME/KEY: CDS		
140	(B)	LOCATION: 1..1431		
142	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 2:		
144	ATG	AAA CAC CTG TGG TTC TTC CTC CTC CTG GTG GCA GCT CCC AGA TGG		48
145	Met	Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp		
W--> 146	240	245	250	
148	GTC	CTG TCC GAG GTG AAG CTG CAG CAG TGG GGC GAA GGA CTT CTG CAG		96
149	Val	Leu Ser Glu Val Lys Leu Gln Gln Trp Gly Glu Gly Leu Leu Gln		
W--> 150	255	260	265	
152	CCT	TCG GAG ACC CTG TCC CGC ACC TGC GTT GTC TCT GGT GGC TCC ATC		144
153	Pro	Ser Glu Thr Leu Ser Arg Thr Cys Val Val Ser Gly Gly Ser Ile		
W--> 154	270	275	280	
156	AGC	GGT TAC TAC TAC TGG ACC TGG ATC CCG CAG ACC CCA GGG AGG GGA		192
157	Ser	Gly Tyr Tyr Tyr Trp Thr Trp Ile Arg Gln Thr Pro Gly Arg Gly		
W--> 158	285	290	295	
160	CTG	GAG TGG ATT GGC CAT ATT TAT GGT AAT GGT GCG ACC ACC AAC TAC		240
161	Leu	Glu Trp Ile Gly His Ile Tyr Gly Asn Gly Ala Thr Thr Asn Tyr		
W--> 162	300	305	310	315
164	AAT	CCC TCC CTC AAG AGT CGA GTC ACC ATT TCA AAA GAC ACG TCC AAG		288
165	Asn	Pro Ser Leu Lys Ser Arg Val Thr Ile Ser Lys Asp Thr Ser Lys		
W--> 166	320	325	330	
168	AAC	CAG TTC CTG AAC TTG AAT TCT GTG ACC GAC GCG GAC ACG GCC		336
169	Asn	Gln Phe Phe Leu Asn Leu Asn Ser Val Thr Asp Ala Asp Thr Ala		
W--> 170	335	340	345	
172	GTC	TAT TAC TGT GCG AGA GGC CCT CGC CCT GAT TGC ACA ACC ATT TGT		384
173	Val	Tyr Tyr Cys Ala Arg Gly Pro Arg Pro Asp Cys Thr Thr Ile Cys		
W--> 174	350	355	360	
176	TAT	GGC GGC TGG GTC GAT GTC TGG GGC CCG GGA GAC CTG GTC ACC GTC		432
177	Tyr	Gly Gly Trp Val Asp Val Trp Gly Pro Gly Asp Leu Val Thr Val		
W--> 178	365	370	375	
180	TCC	TCA GCT AGC ACC AAG GGC CCA TCG GTC TTC CCC CTG GCA CCC TCC		480
181	Ser	Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser		
W--> 182	380	385	390	395
184	TCC	AAG AGC ACC TCT GGG GGC ACA GCG GCC CTG GGC TGC CTG GTC AAG		528
185	Ser	Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys		
W--> 186	400	405	410	
188	GAC	TAC TTC CCC GAA CCG GTG ACC GTG TCG TGG AAC TCA GGC GCC CTG		576
189	Asp	Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu		
W--> 190	415	420	425	
192	ACC	AGC GGC GTG CAC ACC TTC CCG GCT GTC CTA CAG TCC TCA GGA CTC		624

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193	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu
W--> 194	430						435						440			
196	TAC	TCC	CTC	AGC	AGC	GTG	GTG	ACC	GTG	CCC	TCC	AGC	AGC	TTG	GGC	ACC
197	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser	Leu	Gly	Thr	
W--> 198	445						450						455			
200	CAG	ACC	TAC	ATC	TGC	AAC	GTG	AAT	CAC	AAG	CCC	AGC	AAC	ACC	AAG	GTG
201	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	Lys	Pro	Ser	Asn	Thr	Lys	Val
W--> 202	460				465			470			475					
204	GAC	AAG	AAA	GCA	GAG	CCC	AAA	TCT	TGT	GAC	AAA	ACT	CAC	ACA	TGC	CCA
205	Asp	Lys	Lys	Ala	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro
W--> 206					480			485			490					
208	CCG	TGC	CCA	GCA	CCT	GAA	CTC	CTG	GGG	GGA	CCG	TCA	GTC	TTC	CTC	TTC
209	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe
W--> 210					495			500			505					
212	CCC	CCA	AAA	CCC	AAG	GAC	ACC	CTC	ATG	ATC	TCC	CGG	ACC	CCT	GAG	GTC
213	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val
W--> 214					510			515			520					
216	ACA	TGC	GTG	GTG	GAC	GTG	AGC	CAC	GAA	GAC	CCT	GAG	GTC	AAG	TTC	
217	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe
W--> 218					525			530			535					
220	AAC	TGG	TAC	GTG	GAC	GGC	GTG	GAG	GTG	CAT	AAT	GCC	AAG	ACA	AAG	CCG
221	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro
W--> 222	540				545			550			555					
224	CGG	GAG	GAG	CAG	TAC	AAC	AGC	ACG	TAC	CGT	GTG	GTC	AGC	GTC	CTC	ACC
225	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr
W--> 226					560			565			570					
228	GTC	CTG	CAC	CAG	GAC	TGG	CTG	AAT	GGC	AAG	GAG	TAC	AAG	TGC	AAG	GTC
229	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val
W--> 230					575			580			585					
232	TCC	AAC	AAA	GCC	CTC	CCA	GCC	CCC	ATC	GAG	AAA	ACC	ATC	TCC	AAA	GCC
233	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala
W--> 234					590			595			600					
236	AAA	GGG	CAG	CCC	CGA	GAA	CCA	CAG	GTG	TAC	ACC	CTG	CCC	CCA	TCC	CGG
237	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg
W--> 238					605			610			615					
240	GAT	GAG	CTG	ACC	AAG	AAC	CAG	GTC	AGC	CTG	ACC	TGC	CTG	GTC	AAA	GGC
241	Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly
W--> 242					620			625			630			635		
244	TTC	TAT	CCC	AGC	GAC	ATC	GCC	GTG	GAG	TGG	GAG	AGC	AAT	GGG	CAG	CCG
245	Phe	Tyr	Pro	Ser	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	
W--> 246					640			645			650					
248	GAG	AAC	AAC	TAC	AAG	ACC	ACG	CCT	CCC	GTG	CTG	GAC	TCC	GAC	GGC	TCC
249	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser
W--> 250					655			660			665					
252	TTC	TTC	CTC	TAC	AGC	AAG	CTC	ACC	GTG	GAC	AAG	AGC	AGG	TGG	CAG	CAG
253	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln
W--> 254					670			675			680					
256	GGG	AAC	GTC	TTC	TCA	TGC	TCC	GTG	ATG	CAT	GAG	GCT	CTG	CAC	AAC	CAC
257	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His

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W--> 258	685	690	695	
260	TAC ACG CAG AAG AGC CTC TCC CTG TCT CCG GGT AAA TGA			1431
261	Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys *			
W--> 262	700	705	710	
265	(2) INFORMATION FOR SEQ ID NO: 3:			
267	(i) SEQUENCE CHARACTERISTICS:			
268	(A) LENGTH: 720 base pairs			
269	(B) TYPE: nucleic acid			
270	(C) STRANDEDNESS: single			
271	(D) TOPOLOGY: linear			
273	(ii) MOLECULE TYPE: DNA (genomic)			
275	(ix) FEATURE:			
276	(A) NAME/KEY: CDS			
277	(B) LOCATION: 1..720			
279	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:			
281	ATG AGC CTC CCT GCT CAG CTC GGG CTG CTA TTG CTC TGC GTC CCC			48
282	Met Ser Leu Pro Ala Gln Leu Leu Gly Leu Leu Leu Cys Val Pro			
W--> 283	480	485	490	
285	GGG TCC AGT GGG GAA GTT GTG ATG ACT CAG TCT CCA CTG TCC CTT CCC			96
286	Gly Ser Ser Gly Glu Val Val Met Thr Gln Ser Pro Leu Ser Leu Pro			
W--> 287	495	500	505	
289	ATC ACA CCT GGA GAG CCG GCC TCC ATC TCC TGT AGG TCT AGT CAA AGC			144
290	Ile Thr Pro Gly Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser			
W--> 291	510	515	520	525
293	CTT AAA CAC AGT AAT GGA GAC ACC TTC CTG AGT TGG TAT CAG CAG AAG			192
294	Leu Lys His Ser Asn Gly Asp Thr Phe Leu Ser Trp Tyr Gln Gln Lys			
W--> 295	530	535	540	
297	CCA GGC CAA CCT CCA AGG CTC CTG ATT TAT AAG GTT TCT AAC CGG GAC			240
298	Pro Gly Gln Pro Pro Arg Leu Leu Ile Tyr Lys Val Ser Asn Arg Asp			
W--> 299	545	550	555	
301	TCT GGG GTC CCA GAC AGA TTC AGC GGC AGT GGG GCA GGG ACA GAT TTC			288
302	Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ala Gly Thr Asp Phe			
W--> 303	560	565	570	
305	ACA CTG AAA ATC AGC GCA GTG GAG GCT GAA GAT GTT GGG GTT TAT TTC			336
306	Thr Leu Lys Ile Ser Ala Val Glu Ala Glu Asp Val Gly Val Tyr Phe			
W--> 307	575	580	585	
309	TGC GGG CAA GGT ACA AGG ACT CCT CCC ACT TTC GGC GGA GGG ACC AAG			384
310	Cys Gly Gln Gly Thr Arg Thr Pro Pro Thr Phe Gly Gly Thr Lys			
W--> 311	590	595	600	605
313	GTG GAA ATC AAA CGT ACG GTG GCT GCA CCA TCT GTC TTC ATC TTC CCG			432
314	Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro			
W--> 315	610	615	620	
317	CCA TCT GAT GAG CAG TTG AAA TCT GGA ACT GCC TCT GTT GTG TGC CTG			480
318	Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu			
W--> 319	625	630	635	
321	CTG AAT AAC TTC TAT CCC AGA GAG GCC AAA GTA CAG TGG AAG GTG GAT			528
322	Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp			
W--> 323	640	645	650	
325	AAC GCC CTC CAA TCG GGT AAC TCC CAG GAG AGT GTC ACA GAG CAG GAC			576

VERIFICATION SUMMARY

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Input Set : N:\Crf3\RULE60\10073138.raw
Output Set: N:\CRF3\07252002\J073138.raw

L:30 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:31 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:125 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:146 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:150 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:154 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:158 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:162 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:166 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:170 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:174 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:178 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:182 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:186 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:190 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:194 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:198 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:202 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:206 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:210 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:214 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:218 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:222 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:226 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:230 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:234 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:238 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:242 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:246 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:250 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:254 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:258 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:262 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:283 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:287 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:291 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:295 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:299 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:303 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:307 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:311 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:315 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:319 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:323 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:327 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:331 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:335 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:339 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3

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Output Set: N:\CRF3\07252002\J073138.raw

L:360 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4
L:364 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4
L:368 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4
L:372 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4